

# Intraspecific variation influences community network structure: Tracing the roots of interactions to genetics.

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November 10, 2011

## 1 Summary

### 1.1 Study Proposal

- Using existing data of abundances of facilitated species inside and outside of the nurse genotypes, generate an estimate of the dependency of each species to each genotype
- Compare the network facilitation network structure given different abundances of open and closed genotypes:
- Primary Questions:
  1. Is there an overall preponderance of nestedness or modularity?
  2. Are their bio-geographic patterns of network structure?
  3. Are their phylogenetic patterns of network structure (for both the nurse plants and the beneficiary species)?

## 2 Individual level facilitation network models

## 3 Import Data

```
> mywd <- getwd()  
> setwd("data")
```

```

> cush.data <- list()
> for (i in 1:length(dir())) {
+   cush.data[[i]] <- read.csv(dir()[i])
+ }
> names(cush.data) <- paste(lapply(cush.data, function(x) colnames(x)[2]),
+   dir(), sep = "_")
> setwd(mywd)
> as.character(unique(unlist(lapply(cush.data, function(x) x[,
+   4])))))
> for (i in 1:length(cush.data)) {
+   cush.data[[i]][is.na(cush.data[[i]])] <- 0
+ }
> cush.data <- lapply(cush.data, function(x) data.frame(x[, 1:4],
+   rm.spp(x[, 5:ncol(x)], n = 10)))

```

## 4 Build Models

```

> if (run.rii == TRUE) {
+   cush.rii <- list()
+   cush.rii <- lapply(cush.data, function(x) rii(x[, 5:ncol(x)],
+     rep = x[, 3], site = x[, 4], decreasing = FALSE))
+   any(is.na(unlist(cush.rii)))
+   any(as.logical(lapply(cush.rii, function(x) all(x == 0))))
+   names(cush.data)[as.logical(lapply(cush.rii, function(x) all(x ==
+     0)))]
+ } else {
+ }

[1] "Picnophyllum_bryoides_site05.csv" "Azorella_monantha_site23.csv"
[3] "Bolax_gummifera_site24.csv"       "Azorella_monantha_site25.csv"
[5] "Bolax_gummifera_site26.csv"       "Antennaria_umbrinella_site33.csv"
[7] "Phlox_condensata_site62.csv"

```

|                 | Estimate | Std. Error | t value | Pr(> t ) |
|-----------------|----------|------------|---------|----------|
| (Intercept)     | 18.0620  | 2.9575     | 6.11    | 0.0000   |
| unlist(neg.rii) | 0.7130   | 0.1213     | 5.88    | 0.0000   |

## 5 Ratios of Positive and Negative RII

## 6 Network Structure Metrics

### 6.1 Nestedness

```
> cush.zeros <- as.logical(lapply(cush.rii, function(x) all(x ==
+   0)))
> length(cush.rii[cush.zeros != TRUE])/length(cush.rii)

[1] 0.9090909

> if (run.rii == TRUE) {
+   cush.nest <- lapply(cush.rii, function(x) nested(web = abs(x),
+     method = "NODF"))
+ } else {
+ }
> cush.nest <- as.numeric(cush.nest)
> length(cush.nest)

[1] 77

> total.rii <- as.numeric(I(as.numeric(pos.rii) + as.numeric(neg.rii)))
```

|                     | Estimate | Std. Error | t value | Pr(> t ) |
|---------------------|----------|------------|---------|----------|
| (Intercept)         | -0.0129  | 0.1143     | -0.11   | 0.9102   |
| as.numeric(pos.rii) | 0.0296   | 0.0030     | 9.80    | 0.0000   |

## 7 Modularity

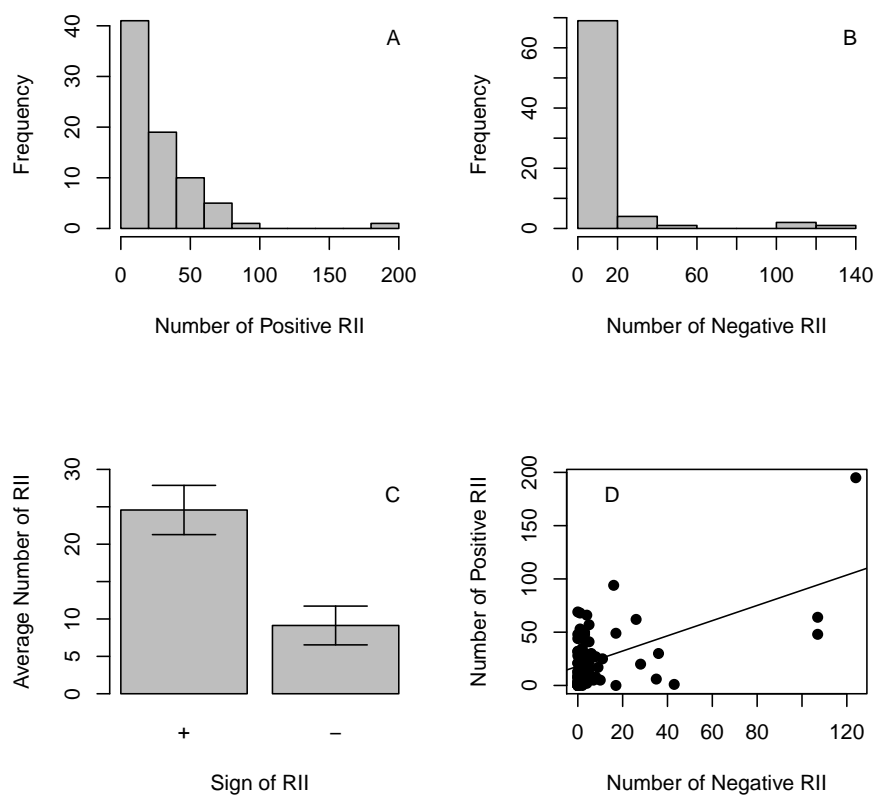


Figure 1:

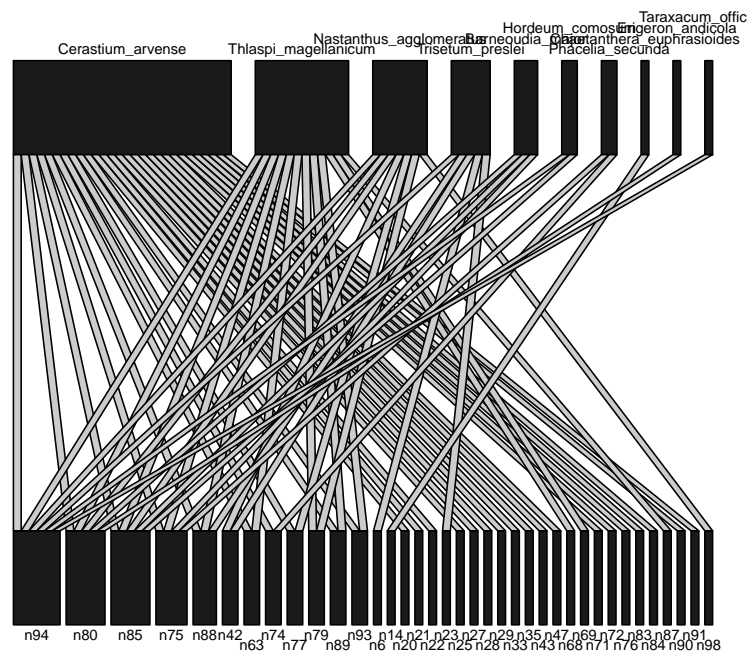


Figure 2:

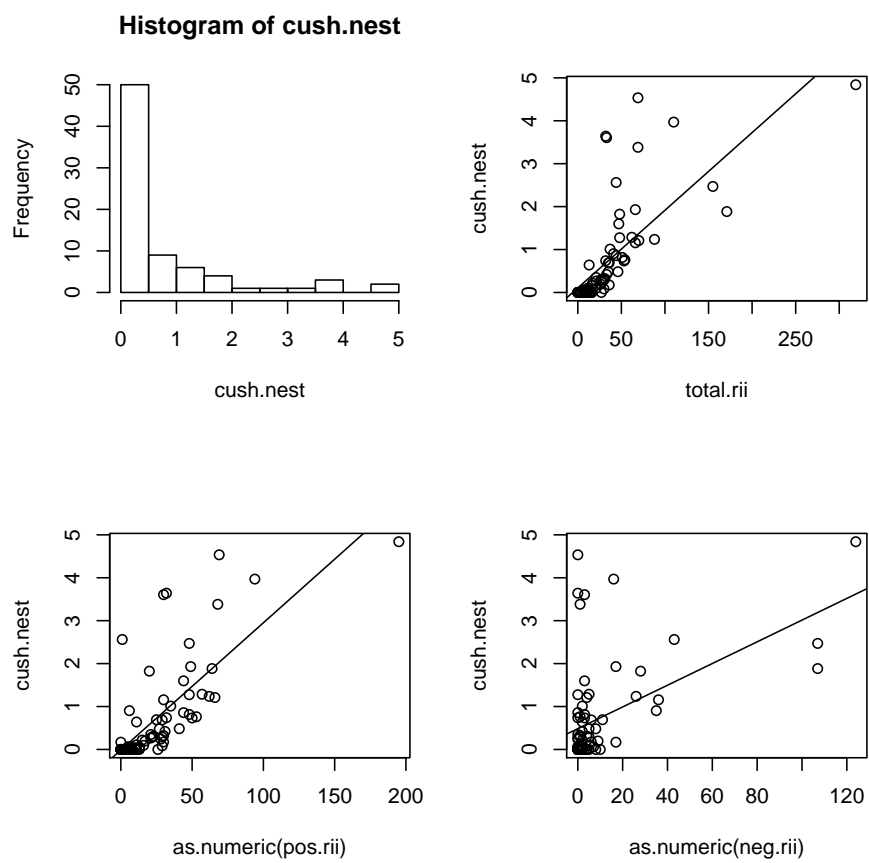


Figure 3:

|                     | Estimate | Std. Error | t value | Pr(> t ) |
|---------------------|----------|------------|---------|----------|
| (Intercept)         | 0.4844   | 0.1221     | 3.97    | 0.0002   |
| as.numeric(neg.rii) | 0.0253   | 0.0050     | 5.05    | 0.0000   |

|             | Estimate | Std. Error | t value | Pr(> t ) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 0.1055   | 0.1126     | 0.94    | 0.3518   |
| total.rii   | 0.0181   | 0.0020     | 9.09    | 0.0000   |